SEQUENCE LISTING

<110>   LUKYANOV, SERGEY A
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        YANUSHEVICH, YURY G

<120>   FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA
        HYDROZOA SPECIES AND METHODS FOR USING SAME

<130>   U 015745-9
<140>   10/532,681
<141>   2005-04-26

<160>   23

<170>   PatentIn version 3.4

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<212>   DNA
<213>   Phialidium sp.

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ggttatggag atgcaagtgt tggtaaagtt gatgcccaat tcatctgcac aactggagat   180

gtaccagttc catggtcaac tttagtaaca acacttactt atggtgcaca atgcttcgcc   240

aaatatggtc cagaattaaa ggatttctac aagagttgca tgcctgaagg ctatgtgcag   300

gagcgtacaa tcacatttga aggggacgga gtatttaaaa ctcgcgctga agttacattt   360

gaaaacggat ctgtttataa ccgagtcaaa cttaatggac aaggatttaa gaaagacgga   420

catgtgcttg aaagaatct tgaattcaat ttcacacctc attgtcttta catttgggga   480

gatcaggcta atcatggttt gaagtctgct ttcaaaatta tgcatgagat tactggatca   540

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<210>   2
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<212>   PRT
<213>   Phialidium sp.

<400>   2

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1   5   10   15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
        20   25   30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
        35   40   45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50   55   60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65   70   75   80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
                85   90   95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
            100   105   110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
            115   120   125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130   135   140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145   150   155   160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe
                165   170   175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180   185   190

Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser
            195   200   205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
    210   215   220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225   230

<210>   3
<211>   705
<212>   DNA
<213>   Artificial sequence

<220>
<223>   phiYFP-Y1 mutant of the phiYFP

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta       180

gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat       240

ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg       300

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gtcaaactta tggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa       420

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cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat       600

atgacatacc atgtcactct cagcaaagat gttactgatc acagggataa catgagcttg       660

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<210> 4
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<213> Artificial sequence

<220>
<223> phiYFP-Y1 mutant of the phiYFP

<400> 4

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Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
            20                  25                  30


Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
        35                  40                  45


Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50                  55                  60


Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65                  70                  75                  80


Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
                85                  90                  95


Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
            100                 105                 110
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Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
        115                 120                 125
```

```
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
        130                 135                 140
```

```
Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145                 150                 155                 160
```

```
Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165                 170                 175
```

```
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
        180                 185                 190
```

```
Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser
        195                 200                 205
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Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
        210                 215                 220
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Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225                 230
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<210>  5
<211>  705
<212>  DNA
<213>  Artificial sequence

<220>
<223>  phiYFP-M0 mutant of the phiYFP

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta     180

gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat     240

ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg     300

acggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga     360

gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa     420

ttcaatttca cacctcattg tctttacatt tggggagatc aggctaatca tggtttgaag     480

tctgctttca aaattcgcca tgagattact ggatcaaaag agacttcat tgttgcagac     540

cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga aaaccatcat     600
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atgagctacc atgtcaagct cagcaaagat gttactgatc acaggatataa catgagcttg   660

aaggaaaccg tacgggctgt ggattgcaga aaaacatatc tttaa   705

<210> 6
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> phiYFP-M0 mutant of the phiYFP

<400> 6

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1   5   10   15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
                20   25   30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
            35   40   45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50   55   60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65   70   75   80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
                85   90   95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
                100   105   110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
            115   120   125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130   135   140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145   150   155   160

Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165   170   175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
                180   185   190

Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser
        195   200   205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
    210   215   220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225   230

<210> 7
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> phiYFP-M1 mutant of the phiYFP

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta   180

gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat   240

ttctacaaga gttgcatgcc tgatggctat gtgcaggagc gtacaatcac atttgaaggg   300

gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga   360

gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa   420

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cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat   600

atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg   660

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<210> 8
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> phiYFP-M1 mutant of the phiYFP

<400> 8

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1   5   10   15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
            20   25   30

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Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
    35              40              45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50              55              60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65              70              75              80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
            85              90              95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
            100             105             110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
    115             120             125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130             135             140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145             150             155             160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
            165             170             175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180             185             190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
    195             200             205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
    210             215             220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225             230
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<210>  9
<211>  705
<212>  DNA
<213>  Artificial sequence

<220>
<223>  humanized version of the phiYFP-M1

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gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc          360

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cacacccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac          600

atgagctacc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg          660

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<210>  10
<211>  234
<212>  PRT
<213>  Artificial sequence

<220>
<223>  humanized version of the phiYFP-M1

<400>  10
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Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1               5                  10                  15


Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
            20                  25                  30


Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
        35                  40                  45


Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50                  55                  60


Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65                  70                  75                  80


Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
                85                  90                  95


Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
            100                 105                 110


Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
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Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130   135   140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145   150   155   160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165   170   175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180   185   190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
        195   200   205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
    210   215   220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225   230

<210> 11
<211> 1047
<212> DNA
<213> Anthomedusae species

<220>
<221> misc_feature
<223> hydromedusa 1 from sub-order Anthomedusae

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ggtgtcaaaa atttacgttc tagaaattgc agtacggaag aaaaacccgt catacttggt   180

gcaatgacag aaacatttca gaaaaaattg ccatataagt tagaattgga tggagatgtt   240

gatgggcaaa catttaaggt tattggtgag ggcgttgggg atgcaaccac tggtgtaatt   300

gaaggaaaat atgtttgtac agaaggagaa gttcctattt catgggtttc gctcatcacc   360

tcattaagtt atggtgcgaa atgttttgtt cgatatccaa atgaaataaa tgattttttc   420

aaaagtactt ttccttctgg atatcatcaa gaaagaaaaa ttacatatga gaatgatggt   480

gttttagaaa cagcagctaa aattactatg gaaagtggtg caatagtgaa tagaataaat   540

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cctccttcga caacatatgt tgttcccgag ggagaaggta ttcgaatcat ctatagaaac   660

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ctttcaacag atccagaaga aaataaagat catattatca tcaaagaaac caactgcgca      840

tttgacgctg attttttctta agatttccga tttgcatcaa gattgaaaaa ctaaataaag      900

ataggtaaaa aaaatatgtc tttgatgtta catacagtat tgatataagc ttcaaagaaa      960

tatattttca aataaacttt ataaaattag gaatctttga atatataaac taaaccttt     1020

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<210> 12
<211> 262
<212> PRT
<213> Anthomedusae species

<220>
<221> misc_feature
<223> hydromedusa 1 from sub-order Anthomedusae

<400> 12

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Gly Val Lys Asn Leu Arg Ser Arg Asn Cys Ser Thr Glu Glu Lys Pro
            20                  25                  30


Val Ile Leu Gly Ala Met Thr Glu Thr Phe Gln Lys Lys Leu Pro Tyr
        35                  40                  45


Lys Leu Glu Leu Asp Gly Asp Val Asp Gly Gln Thr Phe Lys Val Ile
    50                  55                  60


Gly Glu Gly Val Gly Asp Ala Thr Thr Gly Val Ile Glu Gly Lys Tyr
65                  70                  75                  80


Val Cys Thr Glu Gly Glu Val Pro Ile Ser Trp Val Ser Leu Ile Thr
                85                  90                  95


Ser Leu Ser Tyr Gly Ala Lys Cys Phe Val Arg Tyr Pro Asn Glu Ile
            100                 105                 110


Asn Asp Phe Phe Lys Ser Thr Phe Pro Ser Gly Tyr His Gln Glu Arg
            115                 120                 125


Lys Ile Thr Tyr Glu Asn Asp Gly Val Leu Glu Thr Ala Ala Lys Ile
    130                 135                 140


Thr Met Glu Ser Gly Ala Ile Val Asn Arg Ile Asn Val Lys Gly Thr
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145   150   155   160

Gly Phe Asp Lys Asp Gly His Val Cys Gln Lys Asn Leu Glu Ser Ser
            165   170   175

Pro Pro Ser Thr Thr Tyr Val Val Pro Glu Gly Glu Gly Ile Arg Ile
            180   185   190

Ile Tyr Arg Asn Ile Tyr Pro Thr Lys Asp Gly His Tyr Val Val Ala
        195   200   205

Asp Thr Gln Gln Val Asn Arg Pro Ile Arg Ala Gln Gly Thr Ser Ala
    210   215   220

Ile Pro Thr Tyr His His Ile Lys Ser Lys Val Asp Leu Ser Thr Asp
225   230   235   240

Pro Glu Glu Asn Lys Asp His Ile Ile Ile Lys Glu Thr Asn Cys Ala
            245   250   255

Phe Asp Ala Asp Phe Ser
            260

<210>   13
<211>   1089
<212>   DNA
<213>   Anthomedusae species

<220>
<221>   misc_feature
<223>   hydromedusa 2 from sub-order Anthomedusae

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cattatttca atccgatatg acattcaaga tcttcatcga tggagtggtg aatgatcaga   180

aattcacgat aatcgcagat ggatcgtcca aattccccca tggtgacttc aacgtgcatg   240

ctgtgtgcga aaccgggaaa ctcccaatgt catggaaacc tatttgtcac cttatccaat   300

acggggagcc attctttgca aaatatccca atggcatcag ccattttgca caggagtgct   360

ttccagaagg attaacaatt gatcgaacag tcagattcga aaatgacggc actatgacgt   420

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cgacagctga tggtggtctc atgatgtcac attttgattc gaaattgaca ttcaatggtt   660

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cgagagcaat caagattcct ggacctcatt tcgttactgt gataatcaaa cagatgaaag    720

atacaagcga caagcgtgat catgtgtgtc aacgtgaagt cacctacgct cactcagttc    780

cacgcatcac ttctgctatc taaacatcat tcttaaaagg ggaacatgca catcatactt    840

cagtgtgagg gtcagtgtga gggtctttag atgtcaattt gtcgcaggtg tcacacggcg    900

tcgtttagat gttgaaggac gaaatgcgac aaagagatta atagagactc atattttat     960

gtagaatcga ttcattcagc ccattggtaa cctttttggt attttatcat cttattattg    1020

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aagaacttg                                                           1089
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<210>  14
<211>  232
<212>  PRT
<213>  Anthomedusae species

<220>
<221>  misc_feature
<223>  hydromedusa 2 from sub-order Anthomedusae

<400>  14

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
1               5                   10                  15


Phe Ile Asp Gly Val Val Asn Asp Gln Lys Phe Thr Ile Ile Ala Asp
            20                  25                  30


Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
        35                  40                  45


Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
    50                  55                  60


Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His
65                  70                  75                  80


Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val
                85                  90                  95


Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
            100                 105                 110


Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
        115                 120                 125


Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro
    130                 135                 140
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Thr Glu Thr His Met Phe Pro His Gly Ser Asn Ala Val Arg Gln Leu
145             150             155             160


Cys Tyr Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
                165             170             175


Phe Asp Ser Lys Leu Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
            180             185             190


Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser
        195             200             205


Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
    210             215             220


Val Pro Arg Ile Thr Ser Ala Ile
225             230
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<210>  15
<211>  699
<212>  DNA
<213>  Artificial sequence

<220>
<223>  S3-2 mutant of the hm2CP from a hydromedusa 2 from sub-order
       Anthomedusae

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gacggcacta tgacgtctca ccacacctat gagttggacg gcacctgtgt cgtttccagg      360

ataaccgtta attgtgacgg atttcaacct gatggaccaa tcatgagaga ccagcttgtt      420

gatatcctgc aaacgagac acatatgttc cctcatggac ccaatgctgt cagacaattg       480

gctttcatag gcttcacgac agctgatggt ggtctcatga tgtcacattt tgattcgaaa       540

atgacattca atggttcgag agcaatcaag attcctggac ctcatttcgt cactaccata      600

accaaacaga tgaaagatac aagcgacaag cgtgatcatg tgtgtcagcg ggaagtcacc      660

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<210>  16
<211>  232
<212>  PRT
```

<213> Artificial sequence

<220>
<223> S3-2 mutant of the hm2CP from a hydromedusa 2 from sub-order
       Anthomedusae

<400> 16

Met Gln Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
1   5   10   15

Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
                20   25   30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
        35   40   45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
    50   55   60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65   70   75   80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
                85   90   95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
                100   105   110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
        115   120   125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
    130   135   140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145   150   155   160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
                165   170   175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
                180   185   190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
        195   200   205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
    210   215   220

Val Pro Arg Ile Thr Ser Ala Ile
225   230

<210>   17
<211>   705
<212>   DNA
<213>   Artificial sequence

<220>
<223>   phiYFP-M1G1 mutant, derived from humanized version of the
        phiYFP-M1

<400>   17
atgtccagcg gcgccctgct gttccacggc aagatcccct acgtggtgga gatggagggc   60

aatgtggatg gccacacctt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc   120

aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg   180

gtgaccaccc tgtcctacgg cgcccagtgc ttcgccaagt acggccccga gctgaaggat   240

ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc   300

gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc   360

gtgaagctga tggccagggg cttcaagaag gatggccacg tgctgggcaa gaatctggag   420

ttcaatttca cccccactg ccagtacatc tggggcgatc aggccaatca cggcctgaag   480

agcgccttca gatctgcca cgagatcacc ggcagcaagg cgatttcat cgtggccgat   540

cacacccaga tgaataccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac   600

atgagcaccc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg   660

aaggagaccg tgcgcgccgt ggattgccga acagcctacc tgtga   705

<210>   18
<211>   234
<212>   PRT
<213>   Artificial sequence

<220>
<223>   phiYFP-M1G1 mutant, derived from humanized version of the
        phiYFP-M1

<400>   18

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1   5   10   15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
            20   25   30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
        35   40   45

```
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50                  55              60
```

```
Ser Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65                  70              75                      80
```

```
Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
                85              90                      95
```

```
Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
            100             105             110
```

```
Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
        115                 120             125
```

```
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
    130                 135             140
```

```
Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145                 150             155                     160
```

```
Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165             170             175
```

```
Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180             185             190
```

```
Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
        195                 200             205
```

```
Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
    210                 215                 220
```

```
Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu
225                 230
```

```
<210>   19
<211>   705
<212>   DNA
<213>   Artificial sequence

<220>
<223>   phiYFP-M1C1 mutant, derived from humanized version of the
        phiYFP-M1

<400>   19
atgtccagcg cgcccagct gttccacggc aagatcccct acgtggtgga gatggagggc       60

aatgtggatg ccacaccttt cagcatccgc ggcaagggct acggcgatgc cagcgtgggc      120

aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg      180
```

gtgaccaccc tgtcctgggg cgcccagtgc ttcgccaagt acggccccga gctgaaggat   240

ttctacaaga gctgcatgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc   300

gatggcaatt tcaagacccg cgccgaggtg accttcgaga atggcagcgt gtacaatcgc   360

gtgaagctga aggccagggg cttcaagaag gatggccacg tgctgggcaa gaatctggag   420

ttcaatttca cccccccacta ccagtacatc tggggcgatc aggccaatca cggcctgaag   480

agcgccttca gatctgccca cgagatcacc ggcagtaagg cgatttcat cgtggccgat   540

cacacccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccga gtaccaccac   600

atgagcaccc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg   660

aaggagacct tgcgcgccgt ggattgccgc aagacctacc tgtga   705

<210>   20
<211>   234
<212>   PRT
<213>   Artificial sequence

<220>
<223>   phiYFP-M1C1 mutant, derived from humanized version of the
        phiYFP-M1

<400>   20

Met Ser Ser Gly Ala Gln Leu Phe His Gly Lys Ile Pro Tyr Val Val
1   5   10   15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
            20   25   30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
        35   40   45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
    50   55   60

Ser Trp Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65   70   75   80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
                85   90   95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
            100   105   110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Lys Gly Gln Gly Phe
            115   120   125

```
Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
   130                 135                 140


Pro His Tyr Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145                 150                 155                 160


Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
                165                 170                 175


Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
            180                 185                 190


Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
        195                 200                 205


Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu
   210                 215                 220


Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225                 230
```

```
<210>  21
<211>  699
<212>  DNA
<213>  Artificial sequence

<220>
<223>  humanized version of the S3-2 mutant of hm2CP from a hydromedusa
       2 from sub-order Anthomedusae

<400>  21
atggagggcg gccccgccct gttccagagc gacatgacct tcaaaatctt catcgacggc      60

gtggtgaacg gccagaagtt caccatcgtg gccgacggca gcagcaagtt cccccacggc     120

gacttcaacg tgcacgccgt gtgcgagacc ggcaagctgc ccatgagctg gaagcccatc     180

tgccacctga tccagtacgg cgagcccttc ttcgcccgct accccaacgg catcagccac     240

ttcgcccagg agtgcttccc cgagggcctg agcatcgacc gcaccgtgcg cttcgagaac     300

gacggcacca tgaccagcca ccacacctac gagctggacg gcacctgcgt ggtgagccgc     360

atcaccgtga actgcgacgg cttccagccc gacggcccca tcatgcgcga ccagctggtg     420

gacatcctgc ccaacgagac ccacatgttc ccccacggcc ccaacgccgt gcgccagctg     480

gccttcatcg gcttcaccac cgccgacggc ggcctgatga tgagccactt cgacagcaag     540

atgaccttca cggcagccg cgccatcaag atccccggcc cccacttcgt gaccaccatc     600

accaagcaga tgaaggacac cagcgacaag cgcgaccacg tgtgccagcg cgaggtgacc     660

tacgcccaca gcgtgccccg catcaccagc gccatctga                           699
```

```
<210>  22
<211>  232
<212>  PRT
<213>  Artificial sequence

<220>
<223>  humanized S3-2 mutant of hm2CP from a hydromedusa 2 from
       sub-order Anthomedusae

<400>  22
```

Met Gln Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
1   5   10   15

Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
            20   25   30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
        35   40   45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
    50   55   60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65   70   75   80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
                85   90   95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
            100   105   110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
        115   120   125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
    130   135   140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145   150   155   160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
                165   170   175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
            180   185   190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
        195   200   205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
    210   215   220

Val Pro Arg Ile Thr Ser Ala Ile
225   230

<210> 23
<211> 238
<212> PRT
<213> Aequorea victoria

<400> 23

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1   5   10   15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20   25   30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35   40   45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50   55   60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65   70   75   80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85   90   95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
                100   105   110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115   120   125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130   135   140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145   150   155   160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165   170   175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180   185   190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195   200   205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210   215   220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225   230   235